

Figure 1

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1 2 3 4 5 6 7 8 9 10 11 12 13

A

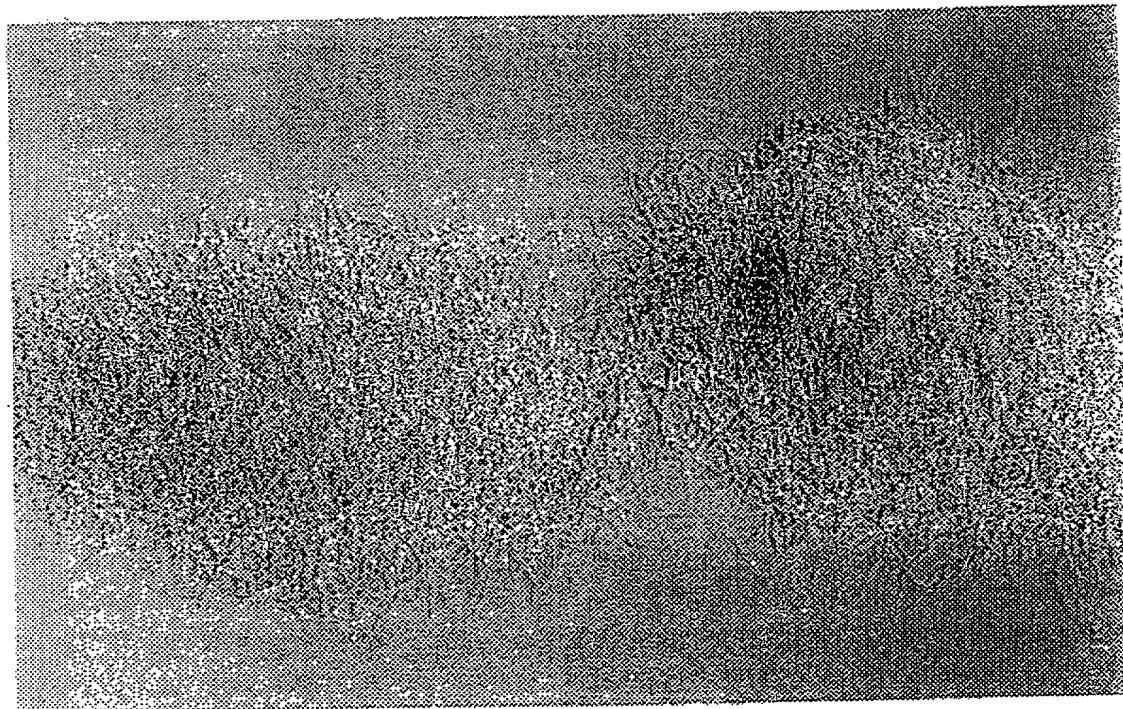


1 2 3 4 5 6 7 8 9 10

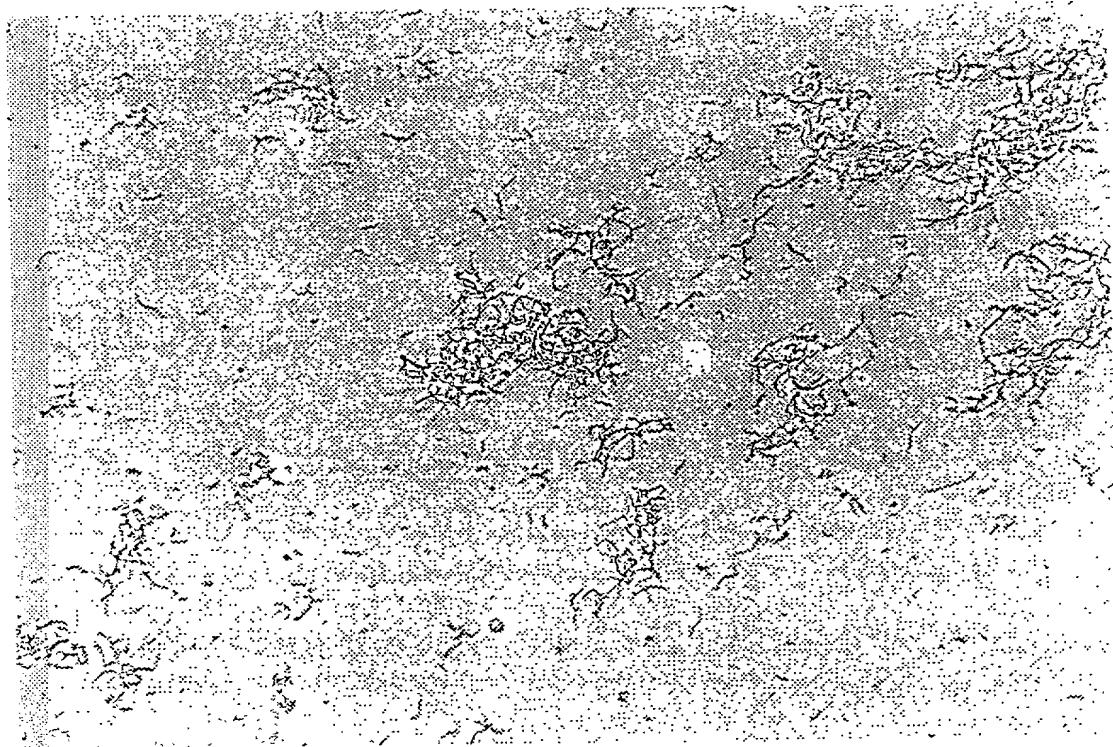
B



Figure 2



A



B

Figure 3

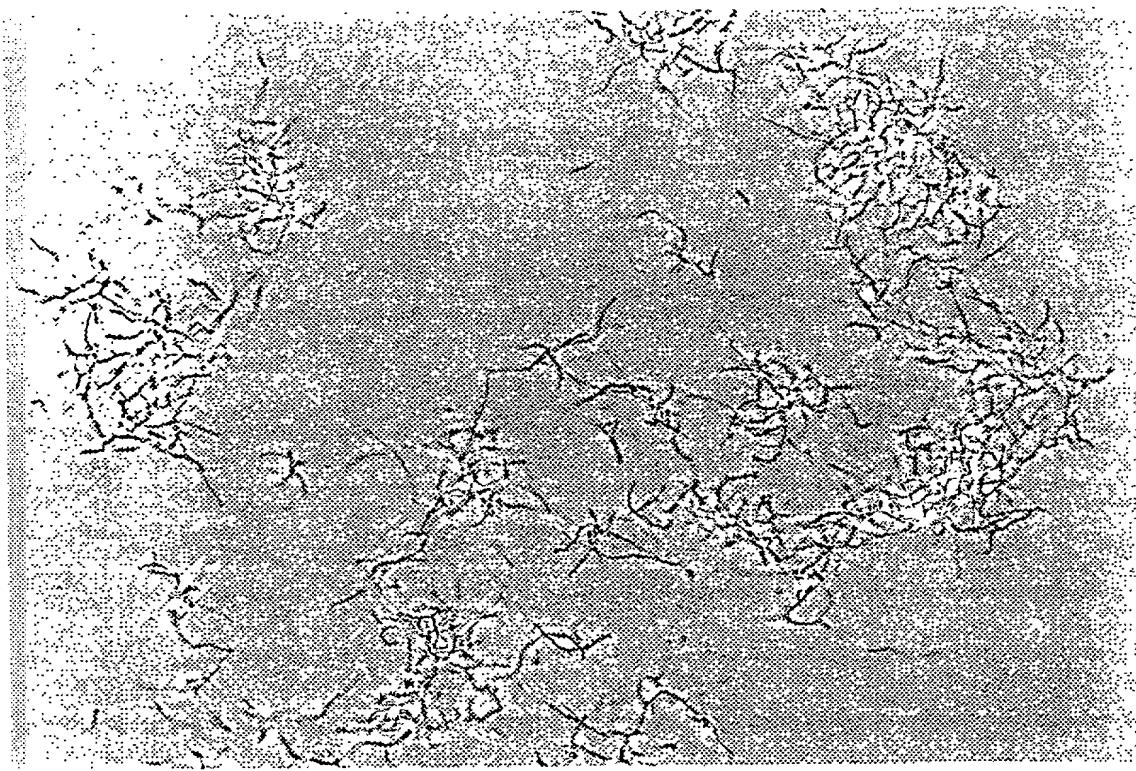
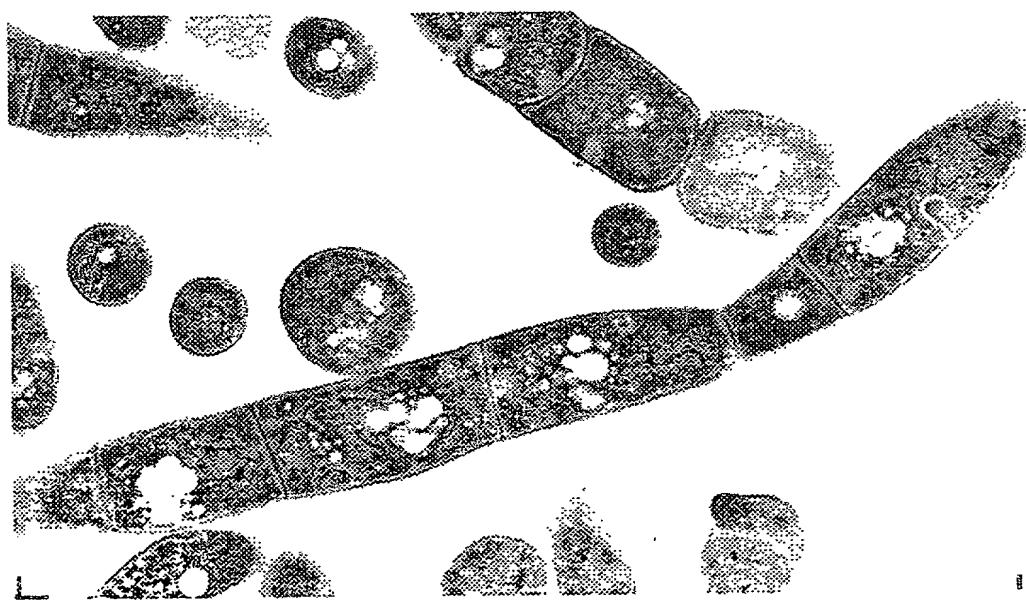
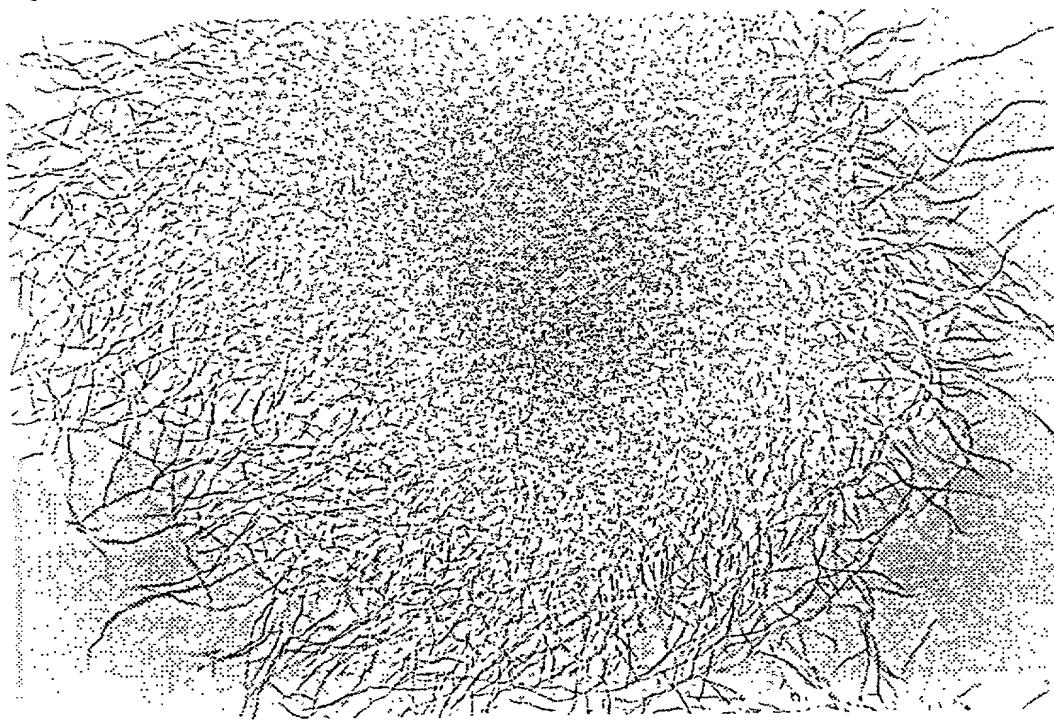
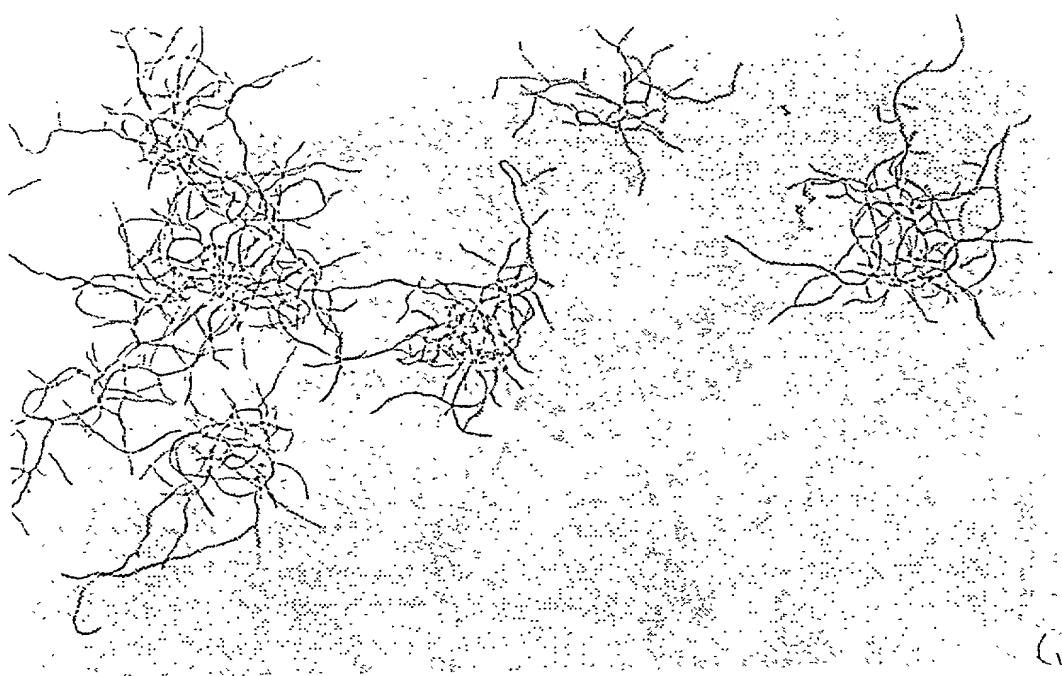


Figure 3C



A



B

Figure 4

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Rijksuniversiteit Leiden
- (B) STREET: Stationsweg 46
- (C) CITY: Leiden
- (D) STATE: Zuid-Holland
- (E) COUNTRY: the Netherlands
- (F) POSTAL CODE (ZIP): 2312 AV

- (A) NAME: Nederlandse Organisatie voor Wetenschappelijk Onderzoek/Chemische Wetenschappen/STW
- (B) STREET: Laan van Nieuw Oost Indie 131
- (C) CITY: The Hague
- (D) STATE: Zuid-Holland
- (E) COUNTRY: the Netherlands
- (F) POSTAL CODE (ZIP): 2593 BM

(ii) TITLE OF INVENTION: Reducing branching and enhancing fragmentation in culturing filamentous microorganisms.

(iii) NUMBER OF SEQUENCES: 13

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(v) CURRENT APPLICATION DATA:

PRIORITY APPLICATION NUMBER : EP 98202148.7

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) Original Source: (A) Organism: Streptomyces griseus
 (B) Strain: ATCC 23345

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..408
- (D) OTHER INFORMATION: /product= "SsgA"
 /gene= "ssgA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATGCGCGAGT CGGTTCAAGC AGAGGTCATG ATGAGCTTCC TCGTCTCCGA GGAGCTCTCG
 60

TTCCGTATTG CGGTGGAGCT CGGATACGAG GTCCGGCGATC CGTATGCCAT CCGGATGACG
 120

Fig. 5

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TTCCACCTTC CCGGCGATGC CCCTGTGACC TGGGCGTTCG GCGCGGAGCT GCTGCTGGAC
180

GGGCTCAACA GCGCGAGCGG CGACGGCGAT GTGCACATCG GCGCGACCGA GCGCGAGGGC
240

CTCGGAGATG TCCACATCCG GCTCCAGGTC GGCAGGGACC GTGCGCTGTT CGGGCGGGG
300

ACGGCACCGC TGGTGGCGTT CCTCGACCGG ACGGACAAGC TCGTGCCTGCT CGGCCAGGAG
360

CACACGCTGG GTGACTTCGA CGGCAACCTG GAGGACGCAC TGGGCCGAT CCTCGCCGAG
420

GAGCAGAACG CGGGCTGA
438

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptomyces griseus
- (B) STRAIN: ATTC 23345

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..408
- (D) OTHER INFORMATION: /product= "SsgA"
/gene= "ssgA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATG AGC TTC CTC GTC TCC GAG GAG CTC TCG TTC CGT ATT CCG GTG GAG
48

Met Ser Phe Leu Val Ser Glu Glu Leu Ser Phe Arg Ile Pro Val Glu
1 5 10 15

CTC CGA TAC GAG GTC GGC GAT CCG TAT GCC ATC CGG ATG ACG TTC CAC
96

Leu Arg Tyr Glu Val Gly Asp Pro Tyr Ala Ile Arg Met Thr Phe His
20 25 30

CTT CCC GGC GAT GCC CCT GTG ACC TGG GCG TTC GGC CGC GAG CTG CTG
144

Leu Pro Gly Asp Ala Pro Val Thr Trp Ala Phe Gly Arg Glu Leu Leu
35 40 45

CTG GAC GGG CTC AAC AGC CCG AGC GGC GAC GGC GAT GTG CAC ATC GGC
192

Leu Asp Gly Leu Asn Ser Pro Ser Gly Asp Gly Asp Val His Ile Gly
50 55 60

CCG ACC GAG CCC GAG GGC CTC GGA GAT GTC CAC ATC CGG CTC CAG GTC

Fig. 5 cont.

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240
 Pro Thr Glu Pro Glu Gly Leu Gly Asp Val His Ile Arg Leu Gln Val
 65 70 75 80
 GGC GCG GAC CGT GCG CTG TTC CGG GCG GGG ACG GCA CCG CTG GTG GCG
 288
 Gly Ala Asp Arg Ala Leu Phe Arg Ala Gly Thr Ala Pro Leu Val Ala
 85 90 95
 TTC CTC GAC CGG ACG GAC AAG CTC GTG CCG CTC GGC CAG GAG CAC ACG
 336
 Phe Leu Asp Arg Thr Asp Lys Leu Val Pro Leu Gly Gln Glu His Thr
 100 105 110
 CTG GGT GAC TTC GAC GGC AAC CTG GAG GAC GCA CTG GGC CGC ATC CTC
 384
 Leu Gly Asp Phe Asp Gly Asn Leu Glu Asp Ala Leu Gly Arg Ile Leu
 115 120 125
 GCC GAG GAG CAG AAC GCC GGC TG
 408
 Ala Glu Glu Gln Asn Ala Gly
 130 135

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Ser Phe Leu Val Ser Glu Glu Leu Ser Phe Arg Ile Pro Val Glu
 1 5 10 15
 Leu Arg Tyr Glu Val Gly Asp Pro Tyr Ala Ile Arg Met Thr Phe His
 20 25 30
 Leu Pro Gly Asp Ala Pro Val Thr Trp Ala Phe Gly Arg Glu Leu Leu
 35 40 45
 Leu Asp Gly Leu Asn Ser Pro Ser Gly Asp Gly Asp Val His Ile Gly
 50 55 60
 Pro Thr Glu Pro Glu Gly Leu Gly Asp Val His Ile Arg Leu Gln Val
 65 70 75 80
 Gly Ala Asp Arg Ala Leu Phe Arg Ala Gly Thr Ala Pro Leu Val Ala
 85 90 95
 Phe Leu Asp Arg Thr Asp Lys Leu Val Pro Leu Gly Gln Glu His Thr
 100 105 110
 Leu Gly Asp Phe Asp Gly Asn Leu Glu Asp Ala Leu Gly Arg Ile Leu
 115 120 125
 Ala Glu Glu Gln Asn Ala Gly
 130 135

(2) INFORMATION FOR SEQ ID NO: 4:

Fig. 5 cont.

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 408 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptomyces albus G
 (B) STRAIN: ATCC 3004

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..408
 (D) OTHER INFORMATION: /product= "SsgA"
 /gene= "ssgA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATG AGC TTC CTC GTC TCC GAG GAG CTC GCC TTC CGC ATC CCG GTG GAG
 48
 Met Ser Phe Leu Val Ser Glu Glu Leu Ala Phe Arg Ile Pro Val Glu
 1 5 10 15
 CTG CGG TAC GAG ACC GTC GAT CCG TAC GCG GTG CGG CTG ACG TTC CAC
 96
 Leu Arg Tyr Glu Thr Val Asp Pro Tyr Ala Val Arg Leu Thr Phe His
 20 25 30
 CTC CCC GGA GAC GCC CCG GTC ACC TGG GTC TTC GGG CGT GAA CTG CTG
 144
 Leu Pro Gly Asp Ala Pro Val Thr Trp Val Phe Gly Arg Glu Leu Leu
 35 40 45
 GTC GAG GGA GTC CTG GAC GCC GCG GGC GAC GGC GAC GTC CGG GTC TGC
 192
 Val Glu Gly Val Leu Asp Ala Ala Gly Asp Gly Asp Val Arg Val Cys
 50 55 60
 CCG GTG GGG CAG ACC GCC ACC AGG GAG GTG CAC ATC ACC CTC CAG GTC
 240
 Pro Val Gly Gln Thr Ala Thr Arg Glu Val His Ile Thr Leu Gln Val
 65 70 75 80
 GGC TCC GAG CAG GCG CTC TTC CGC GTC GGC AAG GCG CCG CTG CTC GCC
 288
 Gly Ser Glu Gln Ala Leu Phe Arg Val Gly Lys Ala Pro Leu Leu Ala
 85 90 95
 TTC CTC GAC CGC ACC GAC CAG GGC TTG TCG CTC GGC AGC GAG CGG GCA
 336
 Phe Leu Asp Arg Thr Asp Gln Gly Leu Ser Leu Gly Ser Glu Arg Ala
 100 105 110
 CAC GCC GAC TTC GAC AGC CAC CTC GAC GAC GCT CTG AAC CGC AGC CTC
 384
 His Ala Asp Phe Asp Ser His Leu Asp Asp Ala Leu Asn Arg Ser Leu
 115 120 125
 GCC GAG GAG CAG AGC GCC GGC TG
 408
 Ala Glu Glu Gln Ser Ala Gly

Fig. 5 cont.

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130

135

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 135 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met	Ser	Phe	Leu	Val	Ser	Glu	Glu	Leu	Ala	Phe	Arg	Ile	Pro	Val	Glu
1				5					10					15	
Leu	Arg	Tyr	Glu	Thr	Val	Asp	Pro	Tyr	Ala	Val	Arg	Leu	Thr	Phe	His
				20				25					30		
Leu	Pro	Gly	Asp	Ala	Pro	Val	Thr	Trp	Val	Phe	Gly	Arg	Glu	Leu	Leu
				35				40				45			
Val	Glu	Gly	Val	Leu	Asp	Ala	Ala	Gly	Asp	Gly	Asp	Val	Arg	Val	Cys
				50				55				60			
Pro	Val	Gly	Gln	Thr	Ala	Thr	Arg	Glu	Val	His	Ile	Thr	Leu	Gln	Val
65					70			75				80			
Gly	Ser	Glu	Gln	Ala	Leu	Phe	Arg	Val	Gly	Lys	Ala	Pro	Leu	Leu	Ala
				85				90				95			
Phe	Leu	Asp	Arg	Thr	Asp	Gln	Gly	Leu	Ser	Leu	Gly	Ser	Glu	Arg	Ala
				100				105				110			
His	Ala	Asp	Phe	Asp	Ser	His	Leu	Asp	Asp	Ala	Leu	Asn	Arg	Ser	Leu
				115			120				125				
Ala	Glu	Glu	Gln	Ser	Ala	Gly									
				130			135								

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 408 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptomyces goldiniensis*
 (B) STRAIN: ATCC 21386

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..408
 (D) OTHER INFORMATION: /product= "SsgA"
 /gene= "ssgA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Fig. 5 cont.

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ATG AGC TTC CTC GTC TCG GAA GAA CTC TCC TTC CGT ATT CCG GTG GAG
 48
 Met Ser Phe Leu Val Ser Glu Glu Leu Ser Phe Arg Ile Pro Val Glu
 1 5 10 15

CTG CGT TAC GAG ACC TGT GAT CCC TAC GCC GTG CGG CTG ACC TTT CAT
 96
 Leu Arg Tyr Glu Thr Cys Asp Pro Tyr Ala Val Arg Leu Thr Phe His
 20 25 30

CTG CCC GGA GAT GCC CCG GTG ACC TGG GCG TTC GGG CGG GAG TTG CTC
 144
 Leu Pro Gly Asp Ala Pro Val Thr Trp Ala Phe Gly Arg Glu Leu Leu
 35 40 45

ATC GAC GGA GGT CCG CGG CCG TGC GGG GAC GGG GAC GTC CAC ATC GCG
 192
 Ile Asp Gly Pro Arg Pro Cys Gly Asp Gly Asp Val His Ile Ala
 50 55 60

CCC GCC GAC CCG GAG ACG TTC GGC GAG GTC CTG ATC CGC CTG CAG GTG
 240
 Pro Ala Asp Pro Glu Thr Phe Gly Glu Val Leu Ile Arg Leu Gln Val
 65 70 75 80

GGG AGC GAC CAG GCG ATG TTC CGG GTC GGC ACG GCG CCG CTG GTG GCC
 288
 Gly Ser Asp Gln Ala Met Phe Arg Val Gly Thr Ala Pro Leu Val Ala
 85 90 95

TTC CTG GAC CGC ACG GAC AAG ATC GTG CCG CTG GGG CAG GAG CGT TCC
 336
 Phe Leu Asp Arg Thr Asp Lys Ile Val Pro Leu Gly Gln Glu Arg Ser
 100 105 110

CTC GCC GAC TTC GAC GCC CTG CTC GAC GAG GCG CTG GAC CGC ATC CTG
 384
 Leu Ala Asp Phe Asp Ala Leu Leu Asp Glu Ala Leu Asp Arg Ile Leu
 115 120 125

GCC GAG GAG CAG AAC GCC GGC TG
 408
 Ala Glu Glu Gln Asn Ala Gly
 130 135

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Ser Phe Leu Val Ser Glu Glu Leu Ser Phe Arg Ile Pro Val Glu
 1 5 10 15

Leu Arg Tyr Glu Thr Cys Asp Pro Tyr Ala Val Arg Leu Thr Phe His
 20 25 30

Leu Pro Gly Asp Ala Pro Val Thr Trp Ala Phe Gly Arg Glu Leu Leu
 35 40 45

Fig. 5 cont.

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Ile Asp Gly Gly Pro Arg Pro Cys Gly Asp Gly Asp Val His Ile Ala
 50 55 60

Pro Ala Asp Pro Glu Thr Phe Gly Glu Val Leu Ile Arg Leu Gln Val
 65 70 75 80

Gly Ser Asp Gln Ala Met Phe Arg Val Gly Thr Ala Pro Leu Val Ala
 85 90 95

Phe Leu Asp Arg Thr Asp Lys Ile Val Pro Leu Gly Gln Glu Arg Ser
 100 105 110

Leu Ala Asp Phe Asp Ala Leu Leu Asp Glu Ala Leu Asp Arg Ile Leu
 115 120 125

Ala Glu Glu Gln Asn Ala Gly
 130 135

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 408 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptomyces netropsis
 - (B) STRAIN: ATCC 23940
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..408
 - (D) OTHER INFORMATION: /product= "SsgA"
/gene= "ssgA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

ATG AGC TTC CTC GTC TCC GAG GAG CTC TCC TTC AAG ATC CCA GTC GAA
 48

Met Ser Phe Leu Val Ser Glu Glu Leu Ser Phe Lys Ile Pro Val Glu
 1 5 10 15

CTG CGA TAC GAG ACC CGG GAT CCC TAC GCG GTG CGG ATG ACC TTC CAC
 96

Leu Arg Tyr Glu Thr Arg Asp Pro Tyr Ala Val Arg Met Thr Phe His
 20 25 30

CTC CCC GGA GAC GCG CCT GTG ACC TGG GCG TTC GCC CGG GAG CTG CTG
 144

Leu Pro Gly Asp Ala Pro Val Thr Trp Ala Phe Gly Arg Glu Leu Leu
 35 40 45

CTC GAC GGG ATC AAC CGC CCG AGC GGC GAC GGC GAC GTC CAC ATC GCC
 192

Leu Asp Gly Ile Asn Arg Pro Ser Gly Asp Gly Asp Val His Ile Ala
 50 55 60

CCG ACC GAC CCC GAG GGC CTG TCG GAC GTC TCC ATC CGG CTC CAG GTG

Fig. 5 cont.

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240
 Pro Thr Asp Pro Glu Gly Leu Ser Asp Val Ser Ile Arg Leu Gln Val
 65 70 75 80

GGC GCG GAC CGC GCC CTC TTC CGT GCA GGC GCC CCG CCG CTG GTC GCC
 288
 Gly Ala Asp Arg Ala Leu Phe Arg Ala Gly Ala Pro Pro Leu Val Ala
 85 90 95

TTC CTC GAC CGC ACG GAC AAG TCG GTG CCG CTC GGT CAG GAA CAG ACT
 336
 Phe Leu Asp Arg Thr Asp Lys Ser Val Pro Leu Gly Gln Glu Gln Thr
 100 105 110

CTG GGT GAC TTC GAG GAC AGC CTG GAG GCC GCG CTC GGC AAG ATC CTC
 384
 Leu Gly Asp Phe Glu Asp Ser Leu Glu Ala Ala Leu Gly Lys Ile Leu
 115 120 125

GCC GAG GAG CAG AAC GCC GGC TG
 408
 Ala Glu Glu Gln Asn Ala Gly
 130 135

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 135 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Met Ser Phe Leu Val Ser Glu Glu Leu Ser Phe Lys Ile Pro Val Glu
 1 5 10 15

Leu Arg Tyr Glu Thr Arg Asp Pro Tyr Ala Val Arg Met Thr Phe His
 20 25 30

Leu Pro Gly Asp Ala Pro Val Thr Trp Ala Phe Gly Arg Glu Leu Leu
 35 40 45

Leu Asp Gly Ile Asn Arg Pro Ser Gly Asp Gly Asp Val His Ile Ala
 50 55 60

Pro Thr Asp Pro Glu GLy Leu Ser Asp Val Ser Ile Arg Leu Gln Val
 65 70 75 80

Gly Ala Asp Arg Ala Leu Phe Arg Ala Gly Ala Pro Pro Leu Val Ala
 85 90 95

Phe Leu Asp Arg Thr Asp Lys Ser Val Pro Leu Gly Gln Glu Gln Thr
 100 105 110

Leu Gly Asp Phe Glu Asp Ser Leu Glu Ala Ala Leu Gly Lys Ile Leu
 115 120 125

Ala Glu Glu Gln Asn Ala Gly
 130 135

(2) INFORMATION FOR SEQ ID NO: 10:

Fig. 5 cont.

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (synthetic)
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL PRODUCT: ssg1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
GGCGAATTCTG AACAGCTACG TGGCGAAGTC GCCA
34

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (synthetic)
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL PRODUCT: ssg2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
GTGGGATCCG TGCTCGCGGC GCTGGTCGTC TC
32

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (synthetic)
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL PRODUCT: ssg3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
GGGAATTCCA TATGCGCGAG TCGGTTCAAG CA
32

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 nucleotides
 - (B) TYPE: nucleic acid

Fig. 5 cont.

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL PRODUCT: ssg4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CCGGTCAGCC GGC GTT CTG C TCCTC
25

Fig. 5 cont.